Figure 1A

Figure 1B
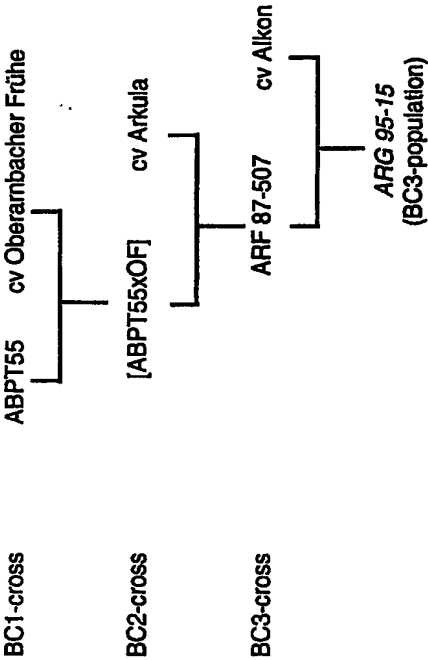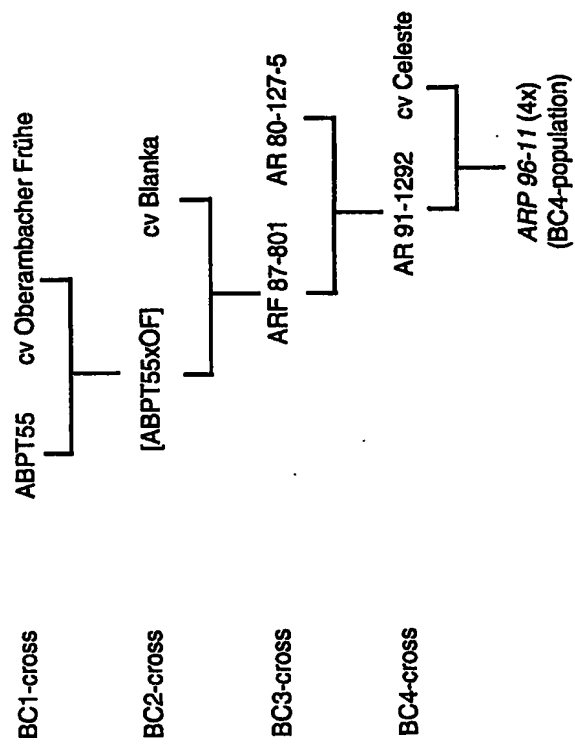
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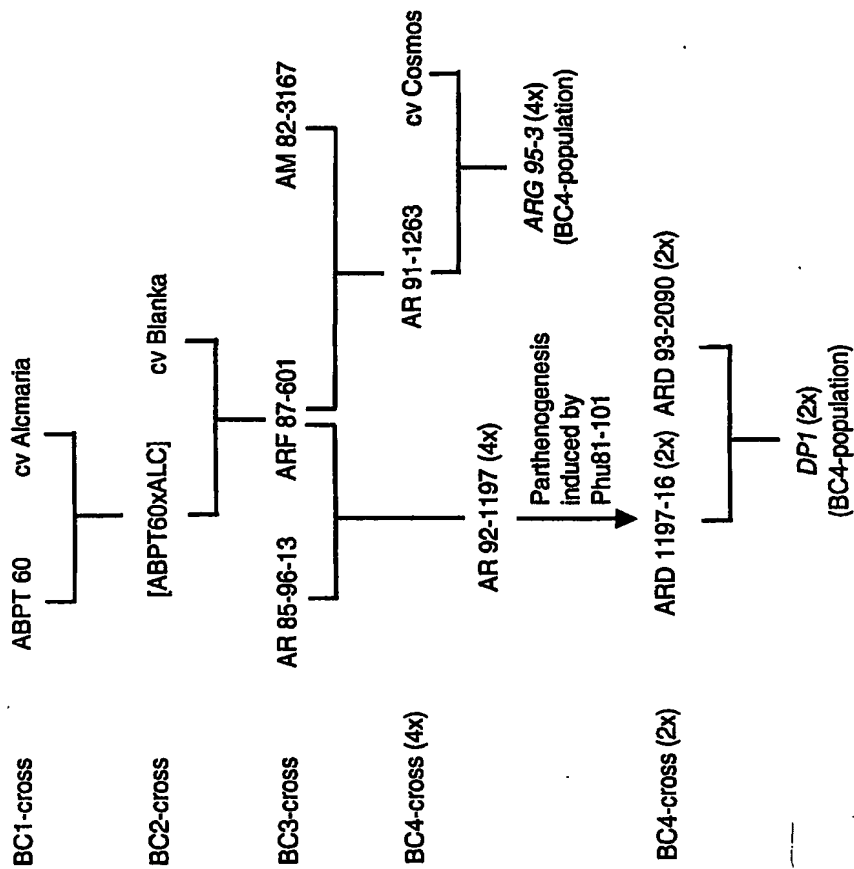
Figure 1D

Figure 2

Figure 3

* ARF 87-507 and ARF 87-601 had identical disease progress curves
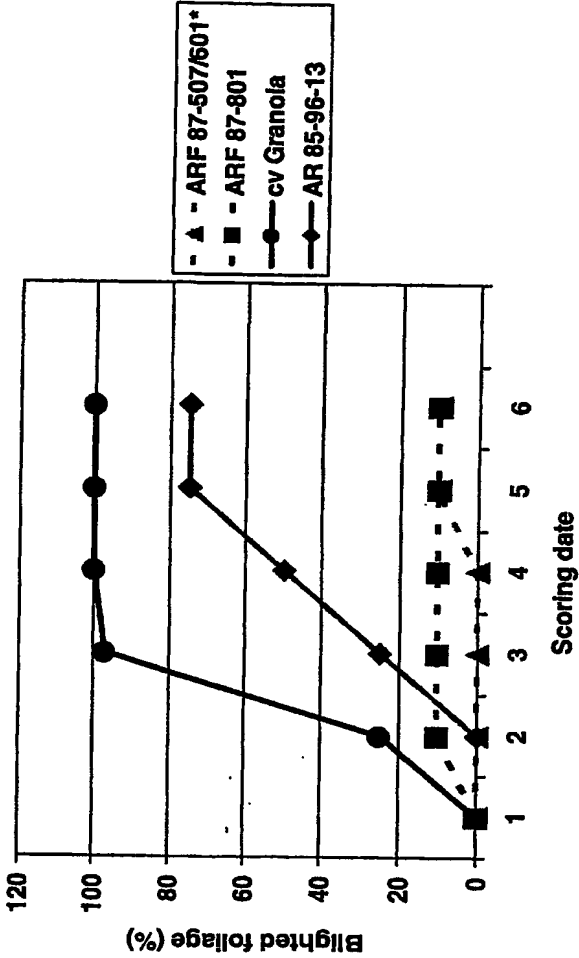
Figure 4

Figure 4 dia 3

Figure 4 dia 4

Figure 4 dia 5

Figure 4 dia 6

Figure 5

Rpi-blb2

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S1E00
E38M50
E40M58
E33M38

E46M61-2

E33M51

E46M61-1

E35M36
E46M52
E38M51
E46M55-2
E33M51#1
E46M55-1
E33M48#2
E33M48#1

1.0 cM

0.7 cM

0.5 cM

2.6 cM

0.6 cM

1.2 cM

0.6 cM
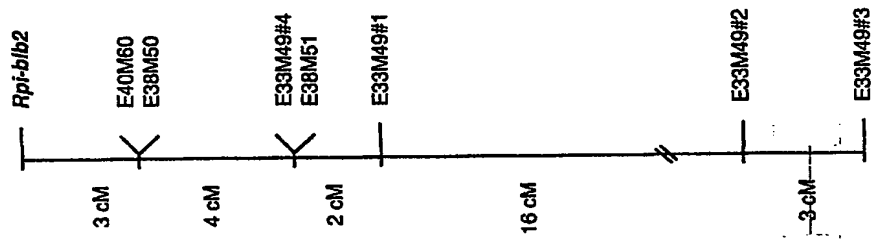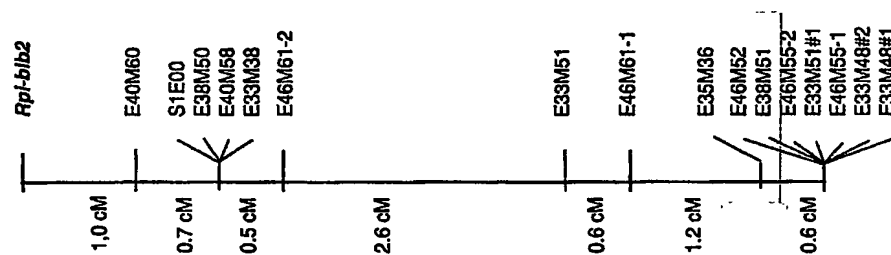
ARG 95-3

Figure 6

Figure 7

Figure 8

Figure 9

Figure 10

Figure 11

Figure 12
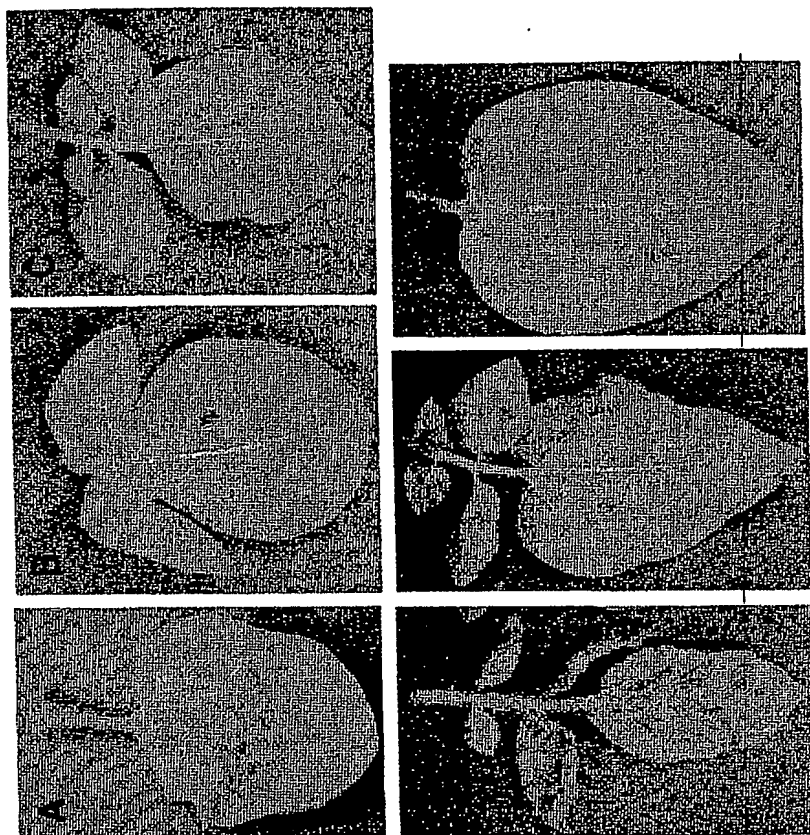
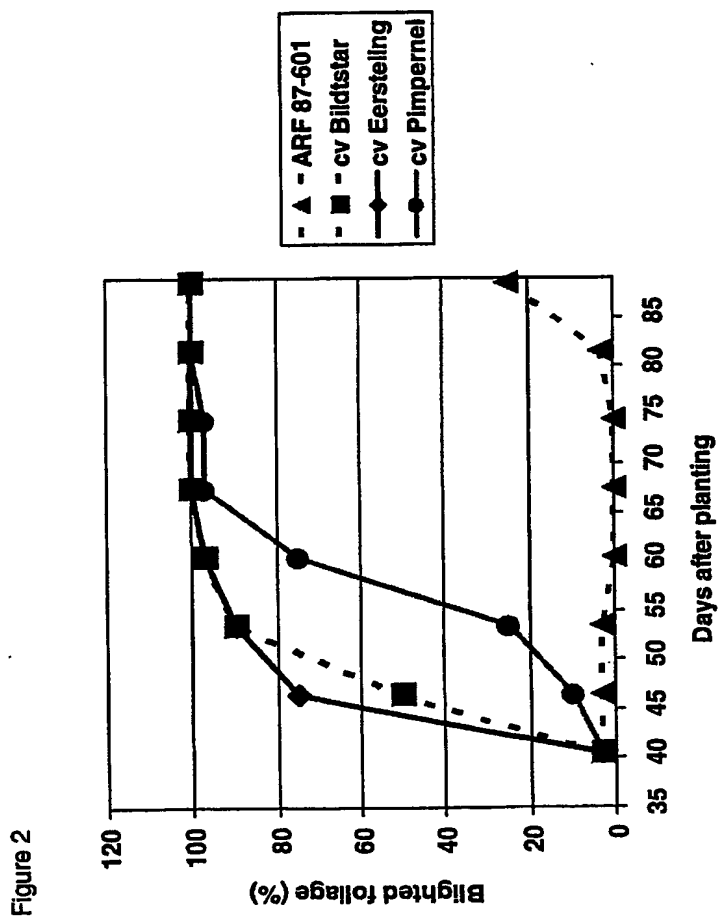Figure 12 dia2
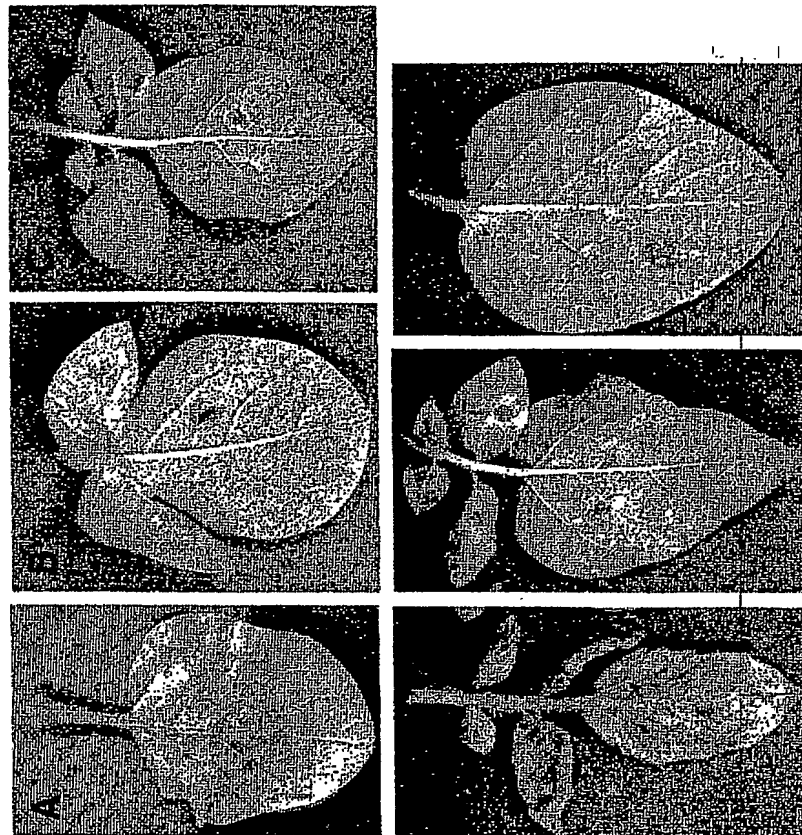
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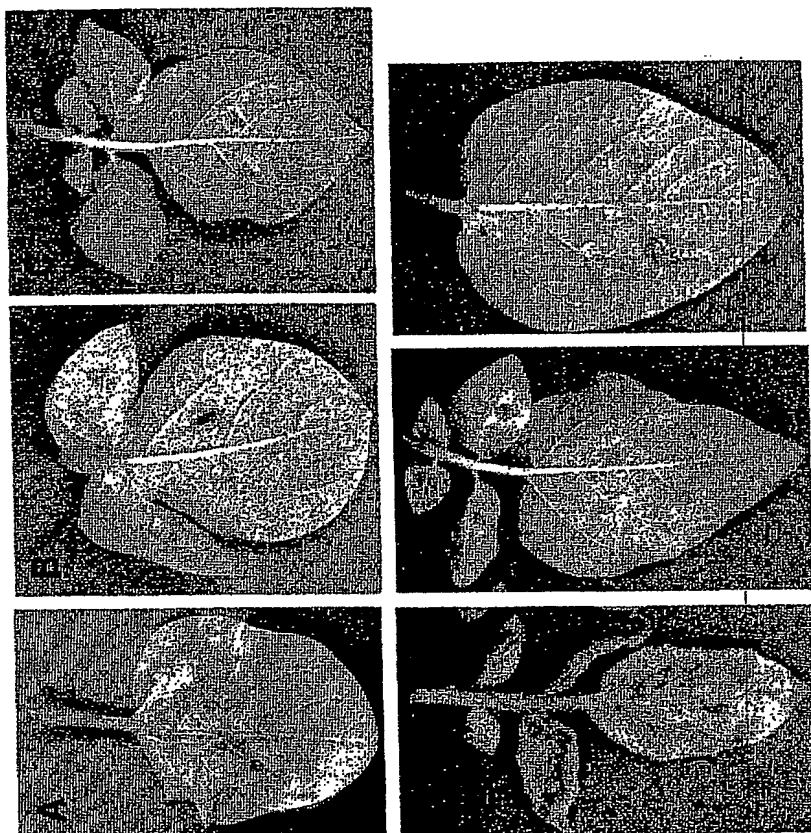
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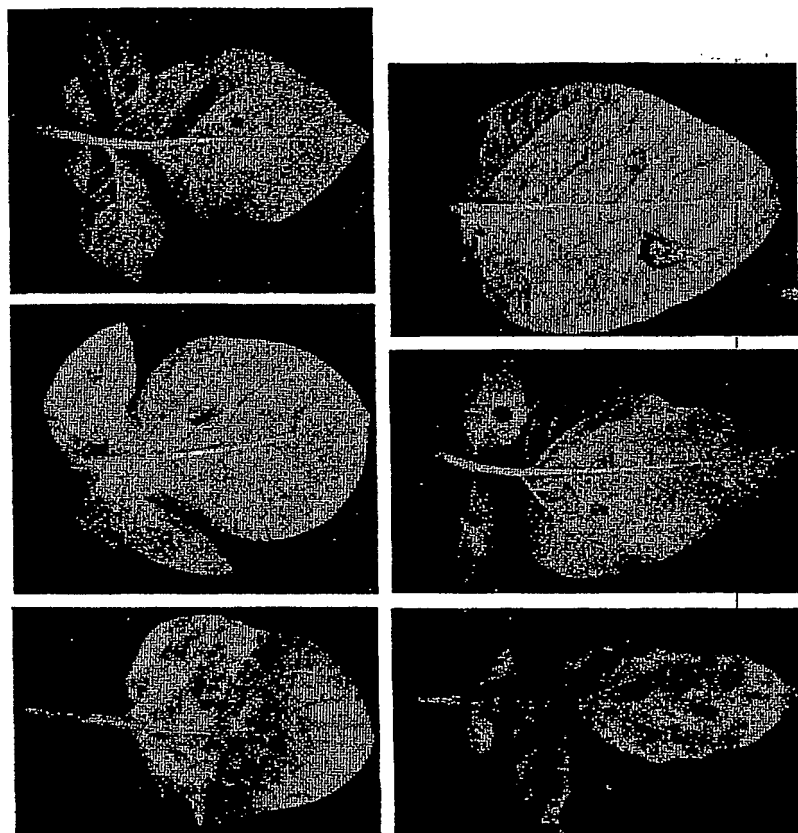
Figure 12 dia 5

Figure 13A

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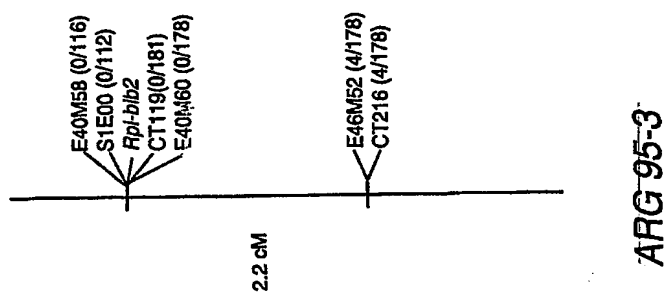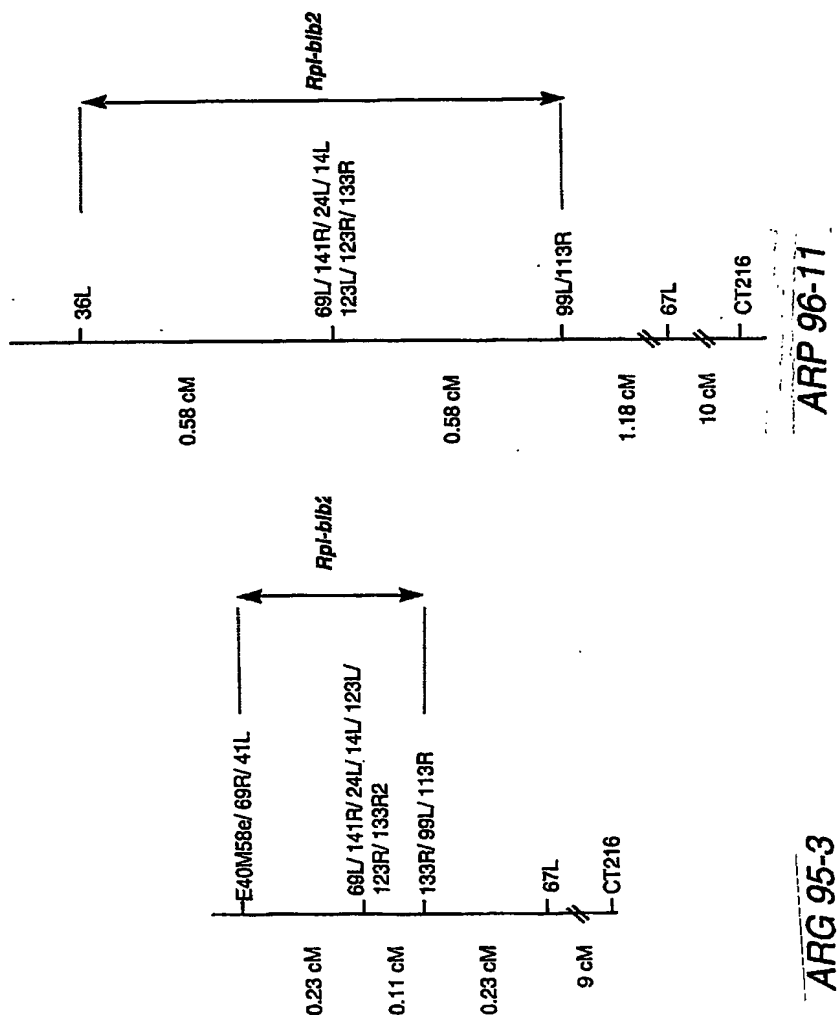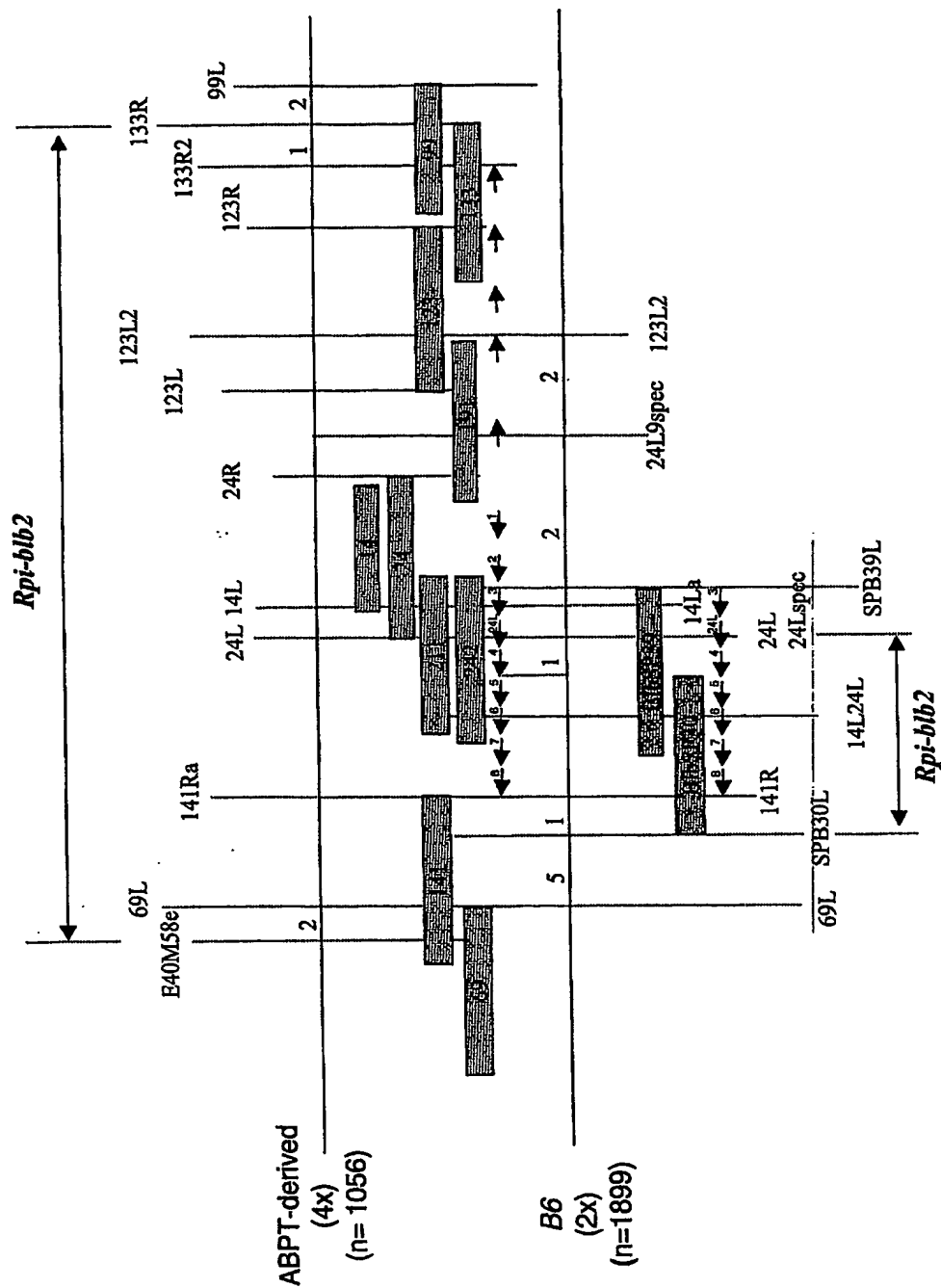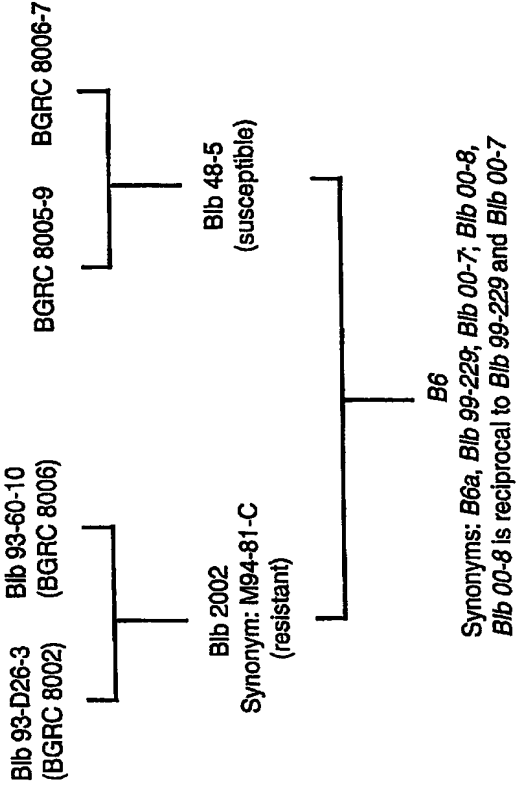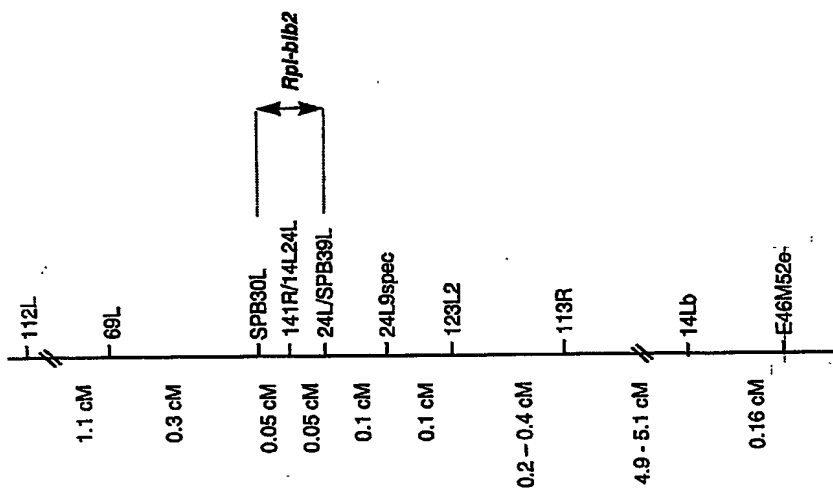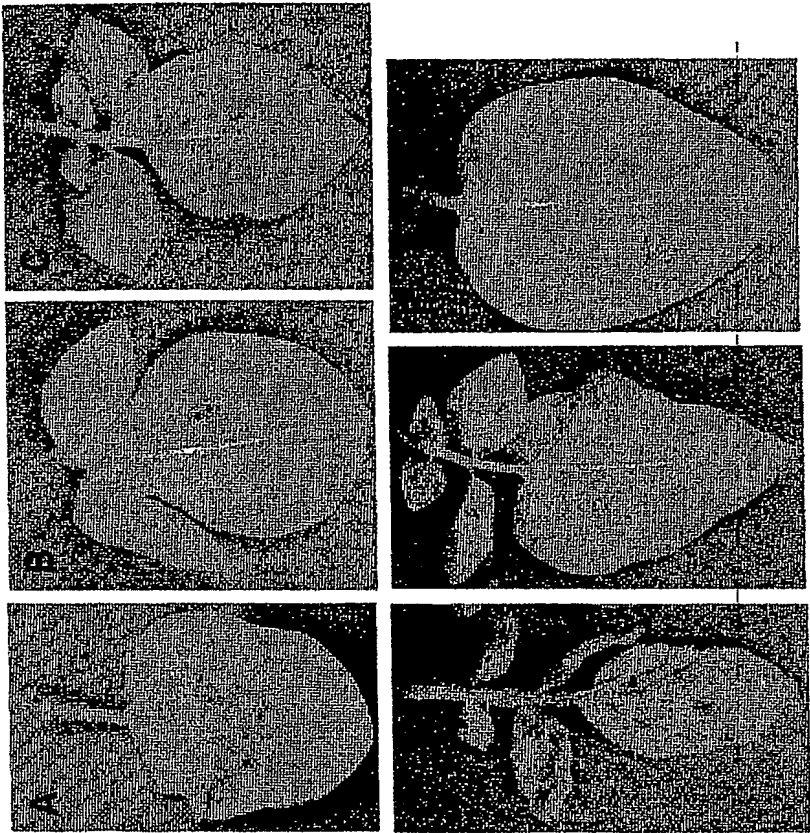
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Figure 13B

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Figure 13C

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Figure 13D

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42/51

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Mi1.1                    VL      S   I   D   V   ---   N   L K QV KI   MA
57
Mi1.2          I         VL      S   I       I   ---   N   L K QV KL   MA
57
Rpi-blb2   MEKRKDNEEANNSLESFSALRKDAANVLDFLERLKNEEDQKAVDVDLIESLKLKLTFICT
60

Mi1.1               C   F Q                   L    --------  F      TS
109
Mi1.2               Y   F Q     · N          SL    --------         TS
109
Rpi-blb2   YVQLSYSDLEKFEDIMTRKRQEVENLLQPILDDDGKDVGCKYVLTSLAGNMDDCISLYHR
120

Mi1.1            Y   I    D    Y   H   I            I              G
169
Mi1.2            Y   I    D    Y   H   I                        L G
169
Rpi-blb2   S-KSDATMMDEQLGFLLLNLSHLSKHRAEKMFPGVTQYEVLQNVCGNIRDFHGLIVNCCI
179

Mi1.1            P       D   H   D T   R       E   R SR
229
Mi1.2            P           H       T R       EH  R SR   Q T
229 Rpi-blb2
       KHEMVENVLSLFQLMAERVGRFLWEDQADEDSQLSELDEDDQNDKDPQLFKLAHLLLKIV 239

Mi1.1            V   I   TN      A V L   Q   .           P   V   S
289
Mi1.2                    TN      A V             I Q       L   P S L
289
Rpi-blb2   PTELEVMHICYKTLKASTSTEIGRFIKKLLETSPDILREYLIHLQEHMITVITPNTSGAR
299

Mi1.1               L       -           D  GV              EP N   GNNQ
348
Mi1.2               L       -              H GT               N   GNNQ
348
Rpi-blb2   NIHVMMEFLLIILSDMPPKDFIHHDKLFDLLARVVALTREVSTLVRDLEEKLRIKESTDE
359

Mi1.1            DL       K      AL    C              HI  N
408
Mi1.2            DL       K      A N   C              HM  N
408
Rpi-blb2   TNCATLKFLENIELLKEDLKHVYLKVPDSSQYCFPMSDGPLFMHLLQRHLDDLLDSNAYS
419

Mi1.1            E E    Q   K      VD-A          A              .
467
Mi1.2      S     E E  SQE          GDAA        I A
468
Rpi-blb2   IALIKEQIGLVKEDLEFIRSFFAN-IEQGLYKDLWERVLDVAYEAKDVIDSIIVRDNGLL
478
           -------------------

Mi1.1            I  IK     I A D   P D   .            R       T   E
527
Mi1.2            I  IK     I A D   P D                R       I   E
528
Rpi-blb2   HLIFSLPITRKKMMLIKEEVSDLHENISKNRGLIVVNSPKKPVESKSLTTDKIIVGFGEE
538

Mi1.1               S       T   S              R           GC
587
```

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```
Mi1.2                      T         S                  R                G    D
588
Rpi-blb2  TNLILRKLTSGPADLDVISIIgmpglgkttlaYKVYNDKSVSSHFDLRAWCTVDQVYDEK
598

Mi1.1      NT  S      D                                      T          ESK
647
Mi1.2       T  S   G D N                                  T  L          EAK
648
Rpi-blb2  KLLDKIFNQVSDSNSKLSENIDVADKLRKQLFGKrylivlddvwDTNTWDELTRPFPDGM
658

Mi1.1                 E       N     D     PD
707
Mi1.2                 E       N     D     PD      D   T
708
Rpi-blb2  KGSRIILTTREKKVALHGKLYTDPLNLRLLRSEESWELLEKRAFGNESCPDELLDVGKEI
718

Mi1.1               A     V     R     QSS S     NS          L       H
767
Mi1.2               A     V     R     QSS S     NS          L       H
768
Rpi-blb2  AENCKglplvvdliagIIAGREKKKSVWLEVVNNLHSFILKNEVEVMKVIEISYDHLPDH
778

Mi1.1             F    TSL  Y  NVYF A     G   E N M       M    Y
827
Mi1.2             H    W    TPL  YLFTVYL A     E   GI       M
828
Rpi-blb2  lkpcllyfasAPKDWVTTIHELKLIWGFEGFVEKTDMKSLEEVVKIYLDDLISSSLVICF
838

Mi1.1       YALNF I         N  F Q  R          T  C EE -
886
Mi1.2       ILNF I          N  F   R          T    EE
888
Rpi-blb2  NEIGDYPTCQlhdlvhdFCLIKARKEKLCDRISSSAPSDLLPRQISIDYDDDEEHFGLNF
898                                                              LRR

Mi1.1      M D         R  I  Q    SV  A          | V  D |HT     →
946                                              |       |
Mi1.2      M D         R     Q    SV  A        I | V  D | P  L   N
948                                              |       |
Rpi-blb2  VLFGSNKKRHSGKHLYSLTINGDELDDHLSDTFHLRHLRLLRTLHLESSFIMVKDSLLNE
958          1              2                    3
Mi1.1          D Q  Y             S   STNR  V     L     R  SVD
1006
Mi1.2          RRQ  Y  F          S   S  G I V    L     R  SVG
1008
Rpi-blb2  ICMLNHLRYLSIGTEVKSLPLSFSNLWNLEILFVDNKESTLILLPRIWDLVKLQVLFTTA
1018           4                5                    6
Mi1.1                        RI T  LI  S   KN     F     L S E
1066
Mi1.2             K          RI    LI  S   MN     F       Q E
1068
Rpi-blb2  CSFFDMDADESILIAEDTKLENLTALGELVLSYWKDTEDIFKRLPNLQVLHFKLKESWDY
1078          7              8                    9
Mi1.1      H  SE        T S G KS          V T      N   I W R
1126
Mi1.2      H   C        T C G KS    HC    VVT      N   E L YD
1128
```

```
Rpi-blb2    STEQYWFPKLDFLTELEKLTVDFERSNTNDSGSSAAINRPWDFHFPSSLKRLQLHEFPLT
1138
                                      10                                    11
Mi1.1                 P       S   H                    F NFN    SI
1186
Mi1.2                 P     N S   D   Q          .     F N RLLT
1188
Rpi-blb2    SDSLSTIARLLNLEELYLYRTIIHGEEWNMGEEDTFENLKCLMLSQVILSKWEVGEESFP
1198
                                    12                    13
Mi1.1       N       K RG   K       P           S KI K      D
1246
Mi1.2       N       K QE GK        P           F KI K      D       K        ND
1248
Rpi-blb2    TLEKLELSDCHNLEEIPSSFGDIYSLKIIELVRSPQLENSALKIKEYAEDMRGGDELQIL
1258
                      14                          15
Mi1.1               N       1255
Mi1.2               N       1257
Rpi-blb2    GQKDIPLFK 1267
```

Figure 16: Multiple Sequence Alignments of Mil.1, Mil.2 and Rpi-blb2 nucleic acids

CLUSTAL W (1.82) Multiple Sequence Alignments

Sequence format is Pearson
Sequence 1: Mil.1   3768 bp
Sequence 2: Mil.2   3774 bp
Sequence 3: Rpi-blb2   3804 bp
Start of Pairwise alignments
Aligning...
Sequences (1:2) Aligned. Score: 95
Sequences (1:3) Aligned. Score: 89
Sequences (2:3) Aligned. Score: 89
Guide tree   file created: [/ebi/extserv/clustalw-work/interactive/clustalw-20040503-
14435620.dnd]
Start of Multiple Alignment
There are 2 groups
Aligning...
Group 1: Sequences: 2   Score:68908
Group 2: Sequences: 3   Score:65855
Alignment Score 66872
CLUSTAL-Alignment file created   [/ebi/extserv/clustalw-work/interactive/clustalw-20040503-
14435620.aln]

CLUSTAL W (1.82) multiple sequence alignment

Figure 17: Multiple Sequence Alignments of Mi1.1, Mi1.2 and Rpi-blb2 proteins

CLUSTAL W (1.82) Multiple Sequence Alignments

Sequence format is Pearson
Sequence 1: Mi1.1   1255 aa
Sequence 2: Mi1.2   1257 aa
Sequence 3: Rpi-blb2   1267 aa
Start of Pairwise alignments
Aligning...
Sequences (1:2) Aligned. Score: 91
Sequences (1:3) Aligned. Score: 82
Sequences (2:3) Aligned. Score: 81
Guide tree   file created: [/ebi/extserv/clustalw-work/interactive/clustalw-20040503-
14322840.dnd]
Start of Multiple Alignment
There are 2 groups
Aligning....
Group 1: Sequences: 2   Score:25939
Group 2: Sequences: 3   Score:24668
Alignment Score 19405
CLUSTAL-Alignment file created [/ebi/extserv/clustalw-work/interactive/clustalw-20040503-
14322840.aln]

CLUSTAL W (1.82) multiple sequence alignment

Mi1.1   MEKRKDNEEANNSLVLFSALSKDIADVLVELE---NEENQKALDKDQVEKIKLKMAFICT 57

```
Mi1.2      MEKRKDIEEAANNSLVLFESALSKDIANVLIFLE---NEENQKALDKDQVEKLKLKMAFICT   57
Rpi-blb2   MEKRKDNEEAANNSLESFESALRKDAANVLDELERLKNEEDQKAVDVDLIESLKLTFICT   60
           ***** ******* **** ** *:** ***    ***:.***:* * .:.***::*:***

Mi1.1      YVQLSCSDFEQFEDIMTRKRQEVENLLQPLLDDD------VETSLTSNMDDCISLYHR   109
Mi1.2      YVQLSYSDFEQFEDIMTRNRQEVENLLQSLLDDD------VLTSLTSNMDDCISLYHR   109
Rpi-blb2   YVQLSYSDLEKFEDIMTRKRQEVENLLQPILDDDGKDVGCKYVLTSLAGNMDDCISLYHR   120
           ***** *** ::********.*:****** :****     .:***** .***********

Mi1.1      SYKSDAIMMDEQLDEFLLLNLYHLSKHHAEKIFPGVTQYEVLQNICGNIRDFHGLIVNGCI   169
Mi1.2      SYKSDAIMMDEQLDEFLLLNLYHLSKHHAEKIFPGVTQYEVLQNVCGNIRDFHGLILNGCI   169
Rpi-blb2   S-KSDATMMDEQLGEFLLLNLSHLSKHRAEKMFPGVTQYEVLQNVCGNIRDFHGLIVNCCI   179
           * **** ******.****** :****:***:*************:*********** * *

Mi1.1      KHEMVENVLPLFQLMADRVGHEFLWDDQTDEDSRLSELDEDEQNDRDSRLFKLAHLLLKIV   229
Mi1.2      KHEMVENVLPLFQLMAERVGHEFLWEDQTDEDSRLSELDEDEHNDRDSRLFQLTHLLLKIV   229
Rpi-blb2   KHEMVENVLSLFQLMAERVGRFLWEDQADEDSQLSELDEDDQNDKDPQLFKLAHLLLKIV   239
           ********* ******:***..***:**:****.*******:.**:** :**:*.*****

Mi1.1      PVELEVIHICYTNLKASTSAEVGLFIKQLLETSPDILREYLIPLQEHMVTVITPSTSGAR   289
Mi1.2      PTELEVMHICYTNLKASTSAEVGRFIKKLLETSPDILREYIIQLQEHMLTVIPPSTLGAR   289
Rpi-blb2   PTELEVMHICYKTLKASTSTEIGRFIKKLLETSPDILREYLIHLQEHMITVITPNTSGAR   299
           *.****:****:.******:*:*:***:************:*:*****:***.*:*.***

Mi1.1      NIHVMMEFLLILSDMP-KDFIHHDKLFEDLLDRVGVLTREVSTLVRDLEEEPRNKEGNNQ   348
Mi1.2      NIHVMMEFLLILSDMP-KDFIHHDKLFEDLLAHVGTLTREVSTLVRDLEEKLRNKEGNNQ   348
Rpi-blb2   NIHVMMEFLLILSDMPPKDFIHHDKLFEDLLARVVALTREVSTLVRDLEEKLRIKESTDE   359
           *************** :********:*****:*  *.:********:***:*:*.. ::.

Mi1.1      TNCATLDLLENIELLKKDLKHVYLKALDSSQCCFPMSDGPLEMHLLHIHLNDLLDSNAYS   408
Mi1.2      TNCATLDLLENIELLKKDLKHVYLKAPNSSQCCFPMSDGPLEMHLLHMHLNDLLDSNAYS   408
```

```
Rpi-blb2   TNCATLKFLENIELLKEDLKHVYLKVPDSSQYCFPMSDGPLFMHLLQRHLDDLLDSNAYS   419
           ***.:*********:************.  .:*** *******************: **:.:**********
```

```
Mi1.1      IALIKEEIELVKQDLKFIRSFFVD-AEQGLYKDLWARVLDVAYEAKDVIDSIIVRDNGLL   467
Mi1.2      ISLIKEEIELVSQELEFIRSFFGDAAEQGLYKDIWARVLDVAYEAKDVIDSIIVRDNGLL   468
Rpi-blb2   IALIKEQIGLVKEDLEFIRSFFAN-IEQGLYKDLWERVLDVAYEAKDVIDSIIVRDNGLL   478
           *:*****:* **.::*::*:**** : ******:.* ************************
```

```
Mi1.1      HLIFSLPITIKKIKLIKEEISALDENIPKDRGLIVVNSPKKPVERKSLTTDKITVGFEEE   527
Mi1.2      HLIFSLPITIKKIKLIKEEISALDENIPKDRGLIVVNSPKKPVERKSLTTDKIIVGFEEE   528
Rpi-blb2   HLIFSLPITRKKMMLIKEEVSDLHENISKNRGLIVVNSPKKPVESKSLTTDKIIVGFGEE   538
           ********** **: ****.:*. :.***  .*.:********** :***:**** *** **
```

```
Mi1.1      TNLILRKLTSGSADLDVISITGMPGSGKTTLAYKVYNDKSVSSRFDLRAWCTVDQGCDEK   587
Mi1.2      TNLILRKLTSGPADLDVISITGMPGSGKTTLAYKVYNDKSVSRHFDLRAWCTVDQGYDDK   588
Rpi-blb2   TNLILRKLTSGPADLDVISIIGMPGLGKTTLAYKVYNDKSVSSHFDLRAWCTVDQVYDEK   598
           ***********.********:****.******************  :***********  *  *
```

```
Mi1.1      KLLNTIFSQVSDSDSKLSENIDVADKLRKQLFGKRYLIVLDDVWDTTTWDELTRPFPESK   647
Mi1.2      KLLDTIFSQVSGSDSNLSENIDVADKLRKQLFGKRYLIVLDDVWDTTTLDELTRPFPEAK   648
Rpi-blb2   KLLDKIFNQVSDSNSKLSENIDVADKLRKQLFGKRYLIVLDDVWDTNTWDELTRPFPDGM   658
           ***: **.***.*.*:**************************************.*  ****** *..:
```

```
Mi1.1      KGSRIILTTREKEVALHGKLNTDPLDLRLLRPDESWELLEKRAFGNESCPDELLDVGKEI   707
Mi1.2      KGSRIILTTREKEVALHGKLNTDPLDLRLLRPDESWELLDKRTFGNESCPDELLDVGKEI   708
Rpi-blb2   KGSRIILTTREKKVALHGKLYTDPLNIRLLRSEESWELLEKRAFGNESCPDELLDVGKEI   718
           ************:******** ***:.:**** :.**** :**::**.* ******************
```

```
Mi1.1      AENCKGLPLVADLIAGVIAGREKKRSVWLEVQSSLSSFILNSEVEVMKVIELSYDHLPHH   767
Mi1.2      AENCKGLPLVADLIAGVIAGREKKRSVWLEVQSSLSSFILNSEVEVMKVIELSYDHLPHH   768
Rpi-blb2   AENCKGLPLVVDLIAGIIAGREKKKSVWLEVVNNLHSFILKNEVEVMKVIEISYDHLPDH   778
           **********.****:********:****** ..*:*****.***********:****** *
```

```
Mi1.1     LKPCLLYFASFPKDTSLTIYELNVYFGAEGFVGKTEMNSMEEVVKIYMDDLIYSSLVICF  827
Mi1.2     LKPCLLHFEASWPKDTPLTIYLFTVYLGAEGFVEKTEMKGIEVVKIYMDDLISSSLVICF  828
Rpi-blb2  LKPCLLYFASAPKDWVTTIHELKLIIWGFEGFVEKTDMKSLEEVVKIYLDDLISSSLVICF  838
          ******* . *****:.:****** .. * *****:. .********:.:******

Mi1.1     NEIGYALNFQIHDLVHDFCLIKARKENLFDQIRSSAPSDLLPRQITIDCDEEE-HFGLNF  886
Mi1.2     NEIGDILNFQIHDLVHDFCLIKARKENLFDRIRSSAPSDLLPRQITIDYDEEEEHFGLNF  888
Rpi-blb2  NEIGDYPTCQLHDLVHDFCLIKARKEKLCDRISSSAPSDLLPRQISIDYDDDEEHFGLNF  898
          ****    . *:************:* *:.* ************** *::.:* ******

Mi1.1     VMFDSNKKRHSGKHLYSLRIIGDQLDDSVSDAFHLRHLLRVLDLHTSFIMVKDSLLNE  946
Mi1.2     VMFDSNKKRHSGKHLYSLRINGDQLDDSVSDAFHLRHLRLIRVLDLEPSLIMVNDSLLNE  948
Rpi-blb2  VLFGSNKKRHSGKHLYSLTINGDELDDHLSDTFHLRHLLRTLHLESSFIMVKDSLLNE  958
          *:*. *************** * **:*** .:**:*** *.*... .:*****:.**

Mi1.1     ICMLNHLRYLSIDTQVKYLPLSFSNLWNLESLFVSTNRSILVLLPRILDIVKLRVLSVDA  1006
Mi1.2     ICMLNHLRYLRIRTQVKYLPESFSNLWNLESLFVSNKGSILVLLPRILPRILDIVKLRVLSVGA  1008
Rpi-blb2  ICMLNHLRYLSIGTEVKSLPLSFSNLWNLEILFVDNKESTLILLPRIWDLIVKLQVLFTTA  1018
          **********  *:.:** **.************ ***...: * *.:****** ***.

Mi1.1     CSFFDMDADESILIAEDTKLENLRIITELLISYKDTKNIFKRFPNLQLLSFELKESWDY  1066
Mi1.2     CSFFDMDADESILIAKDTKLENLRILGELLISYKDTMNIFKRFPNLQVLQFELKESWDY  1068
Rpi-blb2  CSFFDMDADESILIAEDTKLENLTALGELVLSYWKDTEDIFKRLPNLQVLHFKLKESWDY  1078
          **************.:*********. :.** ::**:.:****:.* *.:*********

Mi1.1     STEQHWFESELDFLTELETLSVGFKSSNTNDSGSSVATNRPWDFHFPSNLKILWLREFPLT  1126
Mi1.2     STEQHWFPKLDCLTELETLCVGFKSSNTNHCGSSVVTNRPWDFHFPSNLKELLLYDFPLT  1128
Rpi-blb2  STEQYWFPKLDFLTELELKLTVDFERSNTNDSGSSAAINRPWDFHFPSSLKRIQLHEFPLT  1138
          ****:.**..:** * ***. .:.*. *.: .*** ..:******** .**.:.:: ****
```

```
Mi1.1     SDSLSTIARLPNLEELSLYHTIIHGEEWNMGEEDTFENLKFLNENQVSISKWEVGEESFP 1186
Mi1.2     SDSLSTIARLPNLENLSLYDTIIQGEEWNMGEEDTFENLKFLNLRLLTLSKWEVGEESFP 1188
Rpi-blb2  SDSLSTIARLLNLEELYLYRTIIHGEEWNMGEEDTFENLKCLMISQVILSKWEVGEESFP 1198
          ******** ***:* * ***:* *** ****************** ** :: *********

Mi1.1     NLEKLKLRGCHKLEEIPPSFGDIYSLKSIKIVKSPQLEDSALKIKEYAEDMRGGDELQIL 1246
Mi1.2     NLEKLKLQECGKLEEIPPSFGDIYSLKFIKIVKSPQLEDSALKIKKYAEDMRGGNDLQIL 1248
Rpi-blb2  TLEKLELSDCHNLEEIPSSFGDIYSLKIIELVRSPQLENSALKIKEYAEDMRGGDELQIL 1258
          .****:*  * :***** .******** *:::*****:****** :************

Mi1.1     GQKNIPLFK 1255
Mi1.2     GQKNIPLFK 1257
Rpi-blb2  GQKDIPLFK 1267
          ***:*****
```

Figure 18